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TECH CENTER 1600/2900



1600

RAW SEQUENCE LISTING

DATE: 06/06/2002

PATENT APPLICATION: US/09/380,015B

TIME: 15:18:13

Input Set : A:\sequence.txt

Output Set: N:\CRF3\06062002\I380015B.raw

ENTERED

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Carsten Korth
 8 (ii) TITLE OF INVENTION: Immunological Detection of Prions
 10 (iii) NUMBER OF SEQUENCES: 9
 12 (iv) CORRESPONDENCE ADDRESS:
 13 (A) ADDRESSEE: Kanton Zuerich vertreten durch die Erziehungsdirektion
 14 (B) STREET: Walchetur
 15 (C) CITY: Zuerich
 16 (D) STATE: Zuerich
 17 (E) COUNTRY: Switzerland
 18 (F) ZIP: CH-8090
 20 (v) COMPUTER READABLE FORM:
 21 (A) MEDIUM TYPE: Floppy disk
 22 (B) COMPUTER: IBM PC compatible
 23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 26 (vi) CURRENT APPLICATION DATA:
 C--> 27 (A) APPLICATION NUMBER: US/09/380,015B
 C--> 28 (B) FILING DATE: 23-Aug-1999
 30 (vii) PRIOR APPLICATION DATA:
 31 (A) APPLICATION NUMBER: EP 97102837.8
 32 (B) FILING DATE: 21-FEB-1997

35 (2) INFORMATION FOR SEQ ID NO: 1:

37 (i) SEQUENCE CHARACTERISTICS:
 38 (A) LENGTH: 660 base pairs
 39 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 41 (D) TOPOLOGY: linear
 43 (ii) MOLECULE TYPE: DNA (genomic)
 45 (iii) HYPOTHETICAL: NO
 47 (iv) ANTI-SENSE: NO
 49 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: Bos taurus
 51 (D) DEVELOPMENTAL STAGE: Adult
 53 (vii) IMMEDIATE SOURCE:
 54 (B) CLONE: pbPrP3
 58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 60 ATGAAGAAGC GACCAAAACC TGGAGGAGGA TGGAACTG GGGGAGCCG ATACCCAGGA 60
 62 CAGGGCAGTC CTGGAGGCAA CCGTTATCCA CCTCAGGGAG GGGGTGGCTG GGGTCAGCCC 120
 64 CATGGAGGTG GCTGGGGCCA GCCTCATGGA GGTGGCTGGG GCCAGCCTCA TGGAGGTGGC 180
 66 TGGGGTCAGC CCCATGGTGG TGGCTGGGGA CAGCCACATG GTGGTGGAGG CTGGGGTCAA 240
 68 GGTGGTACCC ACGGTCAATG GAACAAACCC AGTAAGCCAA AAACCAACAT GAAGCATGTG 300

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70 GCAGGAGCTG CTGCAGCTGG AGCAGTGGTA GGGGGCCTTG GTGGCTACAT GCTGGGAAGT 360
72 GCCATGAGCA GGCCTCTTAT ACATTTTGGC AGTGACTATG AGGACCGTTA CTATCGTGAA 420
74 AACATGCACC GTTACCCCAA CCAAGTGTAC TACAGGCCAG TGGATCAGTA TAGTAACCAG 480
76 AACAACTTTG TGCATGACTG TGTC AACATC ACAGTCAAGG AACACACAGT CACCACCACC 540
78 ACCAAGGGGG AGAACTTCAC CGAAACTGAC ATCAAGATGA TGGAGCGAGT GGTGGAGCAA 600
80 ATGTGCATTA CCCAGTACCA GAGAGAATCC CAGGCTTATT ACCAACGAGG GGCAAGTTAA 660

```

83 (2) INFORMATION FOR SEQ ID NO: 2:

85 (i) SEQUENCE CHARACTERISTICS:

86 (A) LENGTH: 219 amino acids

87 (B) TYPE: amino acid

88 (C) STRANDEDNESS: single

89 (D) TOPOLOGY: linear

91 (ii) MOLECULE TYPE: protein

93 (iii) HYPOTHETICAL: YES

95 (iv) ANTI-SENSE: NO

97 (vi) ORIGINAL SOURCE:

98 (A) ORGANISM: Bos taurus

101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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103 Met Lys Lys Arg Pro Lys Pro Gly Gly Gly Trp Asn Thr Gly Gly Ser
104 1 5 10 15
106 Arg Tyr Pro Gly Gln Gly Ser Pro Gly Gly Asn Arg Tyr Pro Pro Gln
107 20 25 30
109 Gly Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
110 35 40 45
112 His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln Pro
113 50 55 60
115 His Gly Gly Gly Trp Gly Gln Pro His Gly Gly Gly Trp Gly Gln
116 65 70 75 80
118 Gly Gly Thr His Gly Gln Trp Asn Lys Pro Ser Lys Pro Lys Thr Asn
119 85 90 95
121 Met Lys His Val Ala Gly Ala Ala Ala Gly Ala Val Val Gly Gly
122 100 105 110
124 Leu Gly Gly Tyr Met Leu Gly Ser Ala Met Ser Arg Pro Leu Ile His
125 115 120 125
127 Phe Gly Ser Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu Asn Met His Arg
128 130 135 140
130 Tyr Pro Asn Gln Val Tyr Tyr Arg Pro Val Asp Gln Tyr Ser Asn Gln
131 145 150 155 160
133 Asn Asn Phe Val His Asp Cys Val Asn Ile Thr Val Lys Glu His Thr
134 165 170 175
136 Val Thr Thr Thr Thr Lys Gly Glu Asn Phe Thr Glu Thr Asp Ile Lys
137 180 185 190
139 Met Met Glu Arg Val Val Glu Gln Met Cys Ile Thr Gln Tyr Gln Arg
140 195 200 205
142 Glu Ser Gln Ala Tyr Tyr Gln Arg Gly Ala Ser
143 210 215

```

145 (2) INFORMATION FOR SEQ ID NO: 3:

147 (i) SEQUENCE CHARACTERISTICS:

148 (A) LENGTH: 33 base pairs

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149         (B) TYPE: nucleic acid
150         (C) STRANDEDNESS: single
151         (D) TOPOLOGY: linear
153     (ii) MOLECULE TYPE: other nucleic acid
154         (A) DESCRIPTION: /desc = "oligonucleotide"
156     (iii) HYPOTHETICAL: NO
158     (iv) ANTI-SENSE: NO
163     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
165 GCGAATTCCA TATGAAGAAG CGACCAAAAC CTG      33
167 (2) INFORMATION FOR SEQ ID NO: 4:
169     (i) SEQUENCE CHARACTERISTICS:
170         (A) LENGTH: 31 base pairs
171         (B) TYPE: nucleic acid
172         (C) STRANDEDNESS: single
173         (D) TOPOLOGY: linear
175     (ii) MOLECULE TYPE: other nucleic acid
176         (A) DESCRIPTION: /desc = "oligonucleotide"
178     (iii) HYPOTHETICAL: NO
180     (iv) ANTI-SENSE: NO
183     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
185 CGGGATCCTA TTAAGTTGCC CCTCGTTGGT A      31
187 (2) INFORMATION FOR SEQ ID NO: 5:
189     (i) SEQUENCE CHARACTERISTICS:
190         (A) LENGTH: 5 amino acids
191         (B) TYPE: amino acid
192         (C) STRANDEDNESS: single
193         (D) TOPOLOGY: linear
195     (ii) MOLECULE TYPE: peptide
197     (iii) HYPOTHETICAL: YES
199     (iv) ANTI-SENSE: NO
204     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
206     Leu Ile His Phe Gly
207     1         5
209 (2) INFORMATION FOR SEQ ID NO: 6:
211     (i) SEQUENCE CHARACTERISTICS:
212         (A) LENGTH: 9 amino acids
213         (B) TYPE: amino acid
214         (C) STRANDEDNESS: single
215         (D) TOPOLOGY: linear
217     (ii) MOLECULE TYPE: peptide
219     (iii) HYPOTHETICAL: YES
221     (iv) ANTI-SENSE: NO
226     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
228     Asp Tyr Glu Asp Arg Tyr Tyr Arg Glu
229     1         5
231 (2) INFORMATION FOR SEQ ID NO: 7:
233     (i) SEQUENCE CHARACTERISTICS:
234         (A) LENGTH: 7 amino acids
235         (B) TYPE: amino acid

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236          (C) STRANDEDNESS: single
237          (D) TOPOLOGY: linear
239      (ii) MOLECULE TYPE: peptide
241      (iii) HYPOTHETICAL: YES
243      (iv) ANTI-SENSE: NO
248      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
250      Gly Ser Asp Tyr Glu Asp Arg
251      1          5
253 (2) INFORMATION FOR SEQ ID NO: 8:
255      (i) SEQUENCE CHARACTERISTICS:
256          (A) LENGTH: 9 amino acids
257          (B) TYPE: amino acid
258          (C) STRANDEDNESS: single
259          (D) TOPOLOGY: linear
261      (ii) MOLECULE TYPE: peptide
263      (iii) HYPOTHETICAL: YES
265      (iv) ANTI-SENSE: NO
270      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
272      Tyr Tyr Arg Pro Val Asp Gln Tyr Ser
273      1          5
275 (2) INFORMATION FOR SEQ ID NO: 9:
277      (i) SEQUENCE CHARACTERISTICS:
278          (A) LENGTH: 13 amino acids
279          (B) TYPE: amino acid
280          (C) STRANDEDNESS: single
281          (D) TOPOLOGY: linear
283      (ii) MOLECULE TYPE: peptide
285      (iii) HYPOTHETICAL: YES
287      (iv) ANTI-SENSE: NO
292      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
294      Cys Ile Thr Gln Tyr Gln Arg Glu Ser Gln Ala Tyr Tyr
295      1          5          10

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VERIFICATION SUMMARY

DATE: 06/06/2002

PATENT APPLICATION: US/09/380,015B

TIME: 15:18:14

Input Set : A:\sequence.txt

Output Set: N:\CRF3\06062002\I380015B.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]